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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/978,600

DATE: 11/28/2001

TIME: 17:13:37

Input Set : A:\09978600.raw.txt

Output Set: N:\CRF3\11212001\I978600.raw

SEQUENCE LISTING

ENTERED

(1) GENERAL INFORMATION:

(i) APPLICANT: HERRNSTADT, CORINNA
PARKER, WILLIAM D.
DAVIS, ROBERT
MILLER, SCOTT W.

(ii) TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
Animal Models for Diseases Associated With Mitochondrial
Defects

(iii) NUMBER OF SEQUENCES: 206

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Kenyon & Kenyon
(B) STREET: 1025 Connecticut Avenue, N.W.
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20036-5405

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

C--> (A) APPLICATION NUMBER: US/09/978,600
C--> (B) FILING DATE: 15-Oct-2001
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/413,740
(B) FILING DATE: 30-MAR-1995
(A) APPLICATION NUMBER: PCT/US95/04063
(B) FILING DATE: 30-MAR-1995

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Bonham, David B.
(B) REGISTRATION NUMBER: 34297
(C) REFERENCE/DOCKET NUMBER: 2105/7

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (202) 429-1776
(B) TELEFAX: (202) 429-0796

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1735 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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69      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
71 AGAGGCCTAA CCCCTGTCTT TAGATTTTAC AGTCCAATGC TCACTCAGC CATTTTACCT      60
73 CACCCCCACT GATGTTTCGCC GACCGTTGAC TATTCTCTAC AAACCACAAA GACATTGGAA      120
75 CACTATACCT ATTATTCGGC GCATGAGCTG GAGTCCTAGG CACAGCTCTA AGCCTCCTTA      180
77 TTCGAGCCGA GCTGGGCCAG CCAGGCAACC TTCTAGGTAA CGACCACATC TACAACGTTA      240
79 TCGTCACAGC CCATGCATTT GTAATAATCT TCTTCATAGT AATACCCATC ATAATCGGAG      300
81 GCTTTGGCAA CTGACTAGTT CCCCTAATAA TCGGTGCCCC CGATATGGCG TTTCCCCGCA      360
83 TAAACAACAT AAGCTTCTGA CTCTTACCTC CCTCTCTCCT ACTCCTGCTC GCATCTGCTA      420
85 TAGTGGAGGC CGGAGCAGGA ACAGGTTGAA CAGTCTACCC TCCCTTAGCA GGGAACTACT      480
87 CCCACCCTGG AGCCTCCGTA GACCTAACCA TCTTCTCCTT ACACCTAGCA GGTGTCTCCT      540
89 CTATCTTAGG GGCCATCAAT TTCATCACA CAATTATCAA TATAAAACCC CCTGCCATAA      600
91 CCCAATACCA AACGCCCCCTC TTCGTCTGAT CCGTCTTAAT CACAGCAGTC CTACTTCTCC      660
93 TATCTCTCCC AGTCTAGCT GCTGGCATCA CTACTACTT AACAGACCGC AACCTCAACA      720
95 CCACCTTCTT CGACCCCGCC GGAGGAGGAG ACCCCATTCT ATACCAACAC CTATTCTGAT      780
97 TTTTCGGTCA CCCTGAAGTT TATATCTTA TCCTACCAGG CTTCGGAATA ATCTCCATA      840
99 TTGTAACCTA CTACTCCGGA AAAAAAGAAC CATTTGGATA CATAGGTATG GTCTGAGCTA      900
101 TGATATCAAT TGGATTCTTA GGGTTTATCG TGTGAGCACA CCATATATTT ACAGTAGGAA      960
103 TAGACGTAGA CACACGAGCA TATTTACCT CCGTACCAT AATCATCGCT ATCCCCACCG      1020
105 GCGTCAAAGT ATTTAGCTGA CTCGCCACAC TCCACGGAAG CAATATGAAA TGATCTGCTG      1080
107 CAGTGCTCTG AGCCCTAGGA TTCATCCTTT TCACCGTAGG TGGCCTGACT GGCATTGTAT      1140
109 TAGCAAACCT ATCAATAGAG ATCGTACTAC ACGACACGTA CTACGTTGTA GCCCACTTCC      1200
111 ACTATGTCCT ATCAATAGGA GCTGTATTG CCATCATAGG AGGCTTCATT CACTGATTTC      1260
113 CCCTATTCTC AGGTACACC CTAGACCAAA CCTACGCCAA AATCCATTTC ACTATCATAT      1320
115 TCATCGGCGT AAATCTAACT TTCTTCCCAC AACACTTTCT CGGCCTATCC GGAATGCCCC      1380
117 GACGTTACTC GGACTACCCC GATGCATACA CCACATGAAA CATCCTATCA TCTGTAGGCT      1440
119 CATTCAATTC TCTAACAGCA GTAATATTAA TAATTTTCAT GATTTGAGAA GCCTTCGCTT      1500
121 CGAAGCGAAA AGTCCTAATA GTAGAAGAAC CCTCCATAAA CCTGGAGTGA CTATATGGAT      1560
123 GCCCCCACC CTACCACACA TTCGAAGAAC CCGTATACAT AAAATCTAGA CAAAAAAGGA      1620
125 AGGAATCGAA CCCCCAAAG CTGGTTTCAA GCCAACCCCA TGGCCTCCAT GACTTTTCA      1680
127 AAAAGGTATT AGAAAAACCA TTTCATAACT TTGTCAAAGT TAAATTATAG GCTAA      1735
129 (2) INFORMATION FOR SEQ ID NO: 2:
131      (i) SEQUENCE CHARACTERISTICS:
132          (A) LENGTH: 854 base pairs
133          (B) TYPE: nucleic acid
134          (C) STRANDEDNESS: double
135          (D) TOPOLOGY: linear
137      (ii) MOLECULE TYPE: other nucleic acid
139      (iii) HYPOTHETICAL: NO
141      (iv) ANTI-SENSE: NO
146      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
148 AGGTATTAGA AAAACCATTT CATAACTTTG TCGTCAAAGT TAAATTATAG GCTAAATCCT      60
150 ATATATCTTA ATGGACATG CAGCGCAAGT AGGTCTACAA GACGCTACTT CCCCTATCAT      120
152 AGAAGAGCTT ATCACCTTTC ATGATCACGC CCTCATAATC ATTTTCCTTA TCTGCTTCCT      180
154 AGTCCTGTAT GCCCTTTTCC TAACACTCAC AACAAAACTA ACTAATACTA ACATCTCAGA      240
156 CGCTCAGGAA ATAGAAACCG TCTGAACAT CCTGCCCCGC ATCATCCTAG TCCTCATCGC      300
158 CCTCCCATCC CTACGCATCC TTTACATAAC AGACGAGGTC AACGATCCCT CCCTTACCAT      360
160 CAAATCAATT GGCCACCAAT GGTACTGAAC CTACGAGTAC ACCGACTACG GCGGACTAAT      420
162 CTTCAACTCC TACATACTTC CCCCATTATT CCTAGAACCA GGCGACCTGC GACTCCTTGA      480
164 CGTTGACAAT CGAGTAGTAC TCCCGATTGA AGCCCCCATT CGTATAATAA TTACATCACA      540

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166 AGACCTCTTG CACTCATGAG CTGTCCCCAC ATTAGGCTTA AAAACAGATG CAATTCCCCGG      600
168 ACGTCTAAAC CAAACCACTT TCACCGCTAC ACGACCGGGG GTATACTACG GTCAATGCTC      660
170 TGAAATCTGT GGAGCAAACC ACAGTTTCAT GCCCATCGTC CTAGAATTAA TTCCCCTAAA      720
172 AATCTTTGAA ATAGGGCCCG TATTTACCCT ATAGCACCCC CTCTACCCCC TCTAGAGCCC      780
174 ACTGTAAAGC TAACCTAGCA TTAACCTTTT AAGTTAAAGA TTAAGAGAAC CAACACCTGT      840
176 TTACAGTGAA ATGC                                         854

178 (2) INFORMATION FOR SEQ ID NO: 3:
180   (i) SEQUENCE CHARACTERISTICS:
181       (A) LENGTH: 954 base pairs
182       (B) TYPE: nucleic acid
183       (C) STRANDEDNESS: double
184       (D) TOPOLOGY: linear
186   (ii) MOLECULE TYPE: other nucleic acid
188   (iii) HYPOTHETICAL: NO
190   (iv) ANTI-SENSE: NO
194   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
196 TCGCTGTCGC CTTAATCCAA GCCTACGTTT TCACACTTCT AGTAAGCCTC TACCTGCACG      60
198 ACAACACATA ATGACCCACC AATCACATGC CTATCATATA GTAAAACCCA GCCCATGACC      120
200 CCTAACAGGG GCCCTCTCAG CCCTCCTAAG TACCTCCGGC CTAGCCATGT GATTTCACTT      180
202 CCACTCCATA ACGCTCCTCA TACTAGGCCT ACTAACCAAC ACACTAACCA TATACCAATG      240
204 ATGGCGCGAT GTAACACGAG AAAGCACATA CCAAGGCCAC CACACACCAC CTGTCCAAAA      300
206 AGGCCTTCGA TACGGGATAA TCCTATTTAT TACCTCAGAA GTTTTTTTCT TCGCAGGATT      360
208 TTTCTGAGCC TTTTACCACT CCAGCCTAGC CCCTACCCCC CAATTAGGAG GGCCTGGCC      420
210 CCGAACAGGC ATCACCCCGC TAAATCCCCT AGAAGTCCCA CTCCTAAACA CATCCGTATT      480
212 ACTCGCATCA GGAGTATCAA TCACCTGAGC TCACCATAGT CTAATAGAAA ACAACCGAAA      540
214 CCAAATAATT CAAGCACTGC TTATTACAAT TTTACTGGGT CTCTATTTTA CCTCCTACA      600
216 GCCTCAGAGT ACTTCGAGTC TCCCTTCACC ATTTCCGACG GCATCTACGG CTCAACATTT      660
218 TTTGTAGCCA CAGGCTTCCA CGGACTTCAC GTCATTATTG GCTCAACTTT CCTCACTATC      720
220 TGCTTCATCC GCCAACTAAT ATTTCACTTT ACATCCAAAC ATCACTTTGG CTTCGAAGCC      780
222 GCCGCCTGAT ACTGGCATTG TGTAGATGTG GTTTGACTAT TTCTGTATGT CTCCATCTAT      840
224 GATGAGGGTC TTAATCTTTT AGTATAAATA GTACCGTTAA CTTCCAATTA ACTAGTTTTG      900
226 ACAACATTCA AAAAAGAGTA ATAACTTCG CCTTATCAAC ACCCAATTTT AATA      954

228 (2) INFORMATION FOR SEQ ID NO: 4:
230   (i) SEQUENCE CHARACTERISTICS:
231       (A) LENGTH: 23 base pairs
232       (B) TYPE: nucleic acid
233       (C) STRANDEDNESS: double
234       (D) TOPOLOGY: linear
236   (ii) MOLECULE TYPE: other nucleic acid
238   (iii) HYPOTHETICAL: NO
240   (iv) ANTI-SENSE: NO
245   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
247 ACCTAGCAGG TGTCTCCTCT ATC                                         23

249 (2) INFORMATION FOR SEQ ID NO: 5:
251   (i) SEQUENCE CHARACTERISTICS:
252       (A) LENGTH: 27 base pairs
253       (B) TYPE: nucleic acid
254       (C) STRANDEDNESS: double
255       (D) TOPOLOGY: linear

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257      (ii) MOLECULE TYPE: other nucleic acid
259      (iii) HYPOTHETICAL: NO
261      (iv) ANTI-SENSE: NO
266      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
268 CAATTTTCATC ACAACAATTA TCAATAT                                27
270 (2) INFORMATION FOR SEQ ID NO: 6:
272      (i) SEQUENCE CHARACTERISTICS:
273          (A) LENGTH: 21 base pairs
274          (B) TYPE: nucleic acid
275          (C) STRANDEDNESS: double
276          (D) TOPOLOGY: linear
278      (ii) MOLECULE TYPE: other nucleic acid
280      (iii) HYPOTHETICAL: NO
282      (iv) ANTI-SENSE: NO
287      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
289 GCCATAACCC AATACCAAAC G                                        21
291 (2) INFORMATION FOR SEQ ID NO: 7:
293      (i) SEQUENCE CHARACTERISTICS:
294          (A) LENGTH: 23 base pairs
295          (B) TYPE: nucleic acid
296          (C) STRANDEDNESS: double
297          (D) TOPOLOGY: linear
299      (ii) MOLECULE TYPE: other nucleic acid
301      (iii) HYPOTHETICAL: NO
303      (iv) ANTI-SENSE: NO
308      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
310 AATCACAGCA GTCCTACTTC TCC                                    23
312 (2) INFORMATION FOR SEQ ID NO: 8:
314      (i) SEQUENCE CHARACTERISTICS:
315          (A) LENGTH: 25 base pairs
316          (B) TYPE: nucleic acid
317          (C) STRANDEDNESS: double
318          (D) TOPOLOGY: linear
320      (ii) MOLECULE TYPE: other nucleic acid
322      (iii) HYPOTHETICAL: NO
324      (iv) ANTI-SENSE: NO
329      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
331 TCACAGCAGT CCTACTTCTC CTATC                                25
333 (2) INFORMATION FOR SEQ ID NO: 9:
335      (i) SEQUENCE CHARACTERISTICS:
336          (A) LENGTH: 26 base pairs
337          (B) TYPE: nucleic acid
338          (C) STRANDEDNESS: double
339          (D) TOPOLOGY: linear
341      (ii) MOLECULE TYPE: other nucleic acid
343      (iii) HYPOTHETICAL: NO
345      (iv) ANTI-SENSE: NO
350      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
352 CAAATCCAT TTCACTATCA TATTCA                                26

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Input Set : A:\09978600.raw.txt
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354 (2) INFORMATION FOR SEQ ID NO: 10:
356     (i) SEQUENCE CHARACTERISTICS:
357         (A) LENGTH: 25 base pairs
358         (B) TYPE: nucleic acid
359         (C) STRANDEDNESS: double
360         (D) TOPOLOGY: linear
362     (ii) MOLECULE TYPE: other nucleic acid
364     (iii) HYPOTHETICAL: NO
366     (iv) ANTI-SENSE: NO
371     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
373 TCATAGAAGA GCTATCACC TTTCA                                     25
375 (2) INFORMATION FOR SEQ ID NO: 11:
377     (i) SEQUENCE CHARACTERISTICS:
378         (A) LENGTH: 24 base pairs
379         (B) TYPE: nucleic acid
380         (C) STRANDEDNESS: double
381         (D) TOPOLOGY: linear
383     (ii) MOLECULE TYPE: other nucleic acid
385     (iii) HYPOTHETICAL: NO
387     (iv) ANTI-SENSE: NO
392     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
394 AGAGCTTATC ACCTTCATG ATCA                                     24
396 (2) INFORMATION FOR SEQ ID NO: 12:
398     (i) SEQUENCE CHARACTERISTICS:
399         (A) LENGTH: 18 base pairs
400         (B) TYPE: nucleic acid
401         (C) STRANDEDNESS: double
402         (D) TOPOLOGY: linear
404     (ii) MOLECULE TYPE: other nucleic acid
406     (iii) HYPOTHETICAL: NO
408     (iv) ANTI-SENSE: NO
413     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
415 TGCCCGCCAT CATCCTAG                                         18
417 (2) INFORMATION FOR SEQ ID NO: 13:
419     (i) SEQUENCE CHARACTERISTICS:
420         (A) LENGTH: 18 base pairs
421         (B) TYPE: nucleic acid
422         (C) STRANDEDNESS: double
423         (D) TOPOLOGY: linear
425     (ii) MOLECULE TYPE: other nucleic acid
427     (iii) HYPOTHETICAL: NO
429     (iv) ANTI-SENSE: NO
434     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
436 TGCCCGCCAT CATCCTAG                                         18
438 (2) INFORMATION FOR SEQ ID NO: 14:
440     (i) SEQUENCE CHARACTERISTICS:
441         (A) LENGTH: 21 base pairs
442         (B) TYPE: nucleic acid
443         (C) STRANDEDNESS: double

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/978,600

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L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]